



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/913,558

DATE: 05/08/2002

TIME: 11:05:45

Input Set : N:\paola\US09913558.raw

Output Set: N:\CRF3\05082002\I913558.raw

1 <110> APPLICANT: Brett P. Monia
 2 Lex M. Cowsert
 3 ISIS PHARMACEUTICALS, INC.
 4 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD5 EXPRESSION
 5 <130> FILE REFERENCE: RTSP-0161
 6 <140> CURRENT APPLICATION NUMBER: US/09/913,558
 7 <141> CURRENT FILING DATE: 2001-08-15
 8 <150> PRIOR APPLICATION NUMBER: US 09/256,492
 9 <151> PRIOR FILING DATE: 1999-02-23
 10 <160> NUMBER OF SEQ ID NOS: 47
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 1597
 14 <212> TYPE: DNA
 15 <213> ORGANISM: Homo sapiens
 16 <220> FEATURE:
 17 <221> NAME/KEY: CDS
 18 <222> LOCATION: (150)..(1547)
 19 <400> SEQUENCE: 1

ENTERED

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20   gcatatggca cttgtgaaga taaatgttac tctcccttt ttaattggaa cttctgctta   60
21   ggacctgtgt atgacgtttc acctgtgacg tggtctttcg gtagccactg actttgagtt   120
22   acaggaaggt ctccgaagat ttgtgtcaa atg acg tca atg gcc agc ttg ttt   173
23                                     Met Thr Ser Met Ala Ser Leu Phe
24                                     1           5
25   tct ttt act agt cca gca gta aag cga ttg ttg ggc tgg aaa caa ggt   221
26   Ser Phe Thr Ser Pro Ala Val Lys Arg Leu Leu Gly Trp Lys Gln Gly
27   10           15           20
28   gat gag gag gag aaa tgg gca gaa aag gca gtt gat gct ttg gtg aag   269
29   Asp Glu Glu Glu Lys Trp Ala Glu Lys Ala Val Asp Ala Leu Val Lys
30   25           30           35           40
31   aaa cta aaa aag aaa aag ggt gcc atg gag gaa ctg gag aaa gcc ttg   317
32   Lys Leu Lys Lys Lys Lys Gly Ala Met Glu Glu Leu Glu Lys Ala Leu
33   45           50           55
34   agc agt cca gga cag ccg agt aaa tgt gtc act att ccc aga tct tta   365
35   Ser Ser Pro Gly Gln Pro Ser Lys Cys Val Thr Ile Pro Arg Ser Leu
36   60           65           70
37   gat gga cgc ctg cag gtt tct cac aga aaa ggc tta ccc cat gtt ata   413
38   Asp Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile
39   75           80           85
40   tat tgt cgt gtt tgg cgc tgg ccg gat ttg cag agt cat cat gag cta   461
41   Tyr Cys Arg Val Trp Arg Trp Pro Asp Leu Gln Ser His His Glu Leu
42   90           95           100
43   aag ccg ttg gat att tgt gaa ttt cct ttt gga tct aag caa aaa gaa   509
44   Lys Pro Leu Asp Ile Cys Glu Phe Pro Phe Gly Ser Lys Gln Lys Glu
  
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45	105	110	115	120	
46	gtt tgt atc aac cca	tac cac tat aag aga	gtg gag agt cca gtc	tta	557
47	Val Cys Ile Asn Pro	Tyr His Tyr Lys Arg	Val Glu Ser Pro Val	Leu	
48		125	130	135	
49	cct cca gta tta gtg	cct cgt cat aat gaa	ttc aat cca caa cac	agc	605
50	Pro Pro Val Leu Val	Pro Arg His Asn Glu	Phe Asn Pro Gln His	Ser	
51		140	145	150	
52	ctt ctg gtt cag ttt	agg aac ctg agc cac	aat gaa cca cac atg	cca	653
53	Leu Leu Val Gln Phe	Arg Asn Leu Ser His	Asn Glu Pro His Met	Pro	
54		155	160	165	
55	caa aat gcc acg ttt	cca gat tct ttc cac	cag ccc aac aac act	cct	701
56	Gln Asn Ala Thr Phe	Pro Asp Ser Phe His	Gln Pro Asn Asn Thr	Pro	
57		170	175	180	
58	ttt ccc tta tct cca	aac agc cct tat ccc	cct tcg cct gct agc	agc	749
59	Phe Pro Leu Ser Pro	Asn Ser Pro Tyr Pro	Pro Ser Pro Ala Ser	Ser	
60		185	190	195	200
61	aca tat ccc aac tcc	cca gca agt tct gga	cca gga agt cca ttt	cag	797
62	Thr Tyr Pro Asn Ser	Pro Ala Ser Ser Gly	Pro Gly Ser Pro Phe	Gln	
63		205	210	215	
64	ctc cca gct gat acg	cct cct cct gcc tat	atg cca cct gat gat	cag	845
65	Leu Pro Ala Asp Thr	Pro Pro Pro Ala Tyr	Met Pro Pro Asp Asp	Gln	
66		220	225	230	
67	atg ggt caa gat aat	tcc cag cct atg gat	aca agc aat aat atg	att	893
68	Met Gly Gln Asp Asn	Ser Gln Pro Met Asp	Thr Ser Asn Asn Met	Ile	
69		235	240	245	
70	cct cag att atg ccc	agt ata tcc agc agg	gat gtt cag cct gtt	gcc	941
71	Pro Gln Ile Met Pro	Ser Ile Ser Ser Arg	Asp Val Gln Pro Val	Ala	
72		250	255	260	
73	tat gaa gag cct aaa	cat tgg tgt tca ata	gtc tac tat gaa tta	aac	989
74	Tyr Glu Glu Pro Lys	His Trp Cys Ser Ile	Val Tyr Tyr Glu Leu	Asn	
75		265	270	275	280
76	aat cgt gtt gga gaa	gct ttt cat gca tct	tct act agt gtg tta	gta	1037
77	Asn Arg Val Gly Glu	Ala Phe His Ala Ser	Ser Ser Thr Ser Val	Leu Val	
78		285	290	295	
79	gat gga ttc aca gat	cct tca aat aac aaa	agt aga ttc tgc ttg	ggg	1085
80	Asp Gly Phe Thr Asp	Pro Ser Asn Asn Lys	Ser Arg Phe Cys Leu	Gly	
81		300	305	310	
82	ttg ttg tca aat gtt	aat cgt aat tcg aca	att gaa aac act agg	cga	1133
83	Leu Leu Ser Asn Val	Asn Arg Asn Ser Thr	Ile Glu Asn Thr Arg	Arg	
84		315	320	325	
85	cat att gga aaa ggt	gtt cat ctg tac tat	gtt ggt gga gag gtg	tat	1181
86	His Ile Gly Lys Gly	Val His Leu Tyr Tyr	Val Gly Gly Glu Val	Tyr	
87		330	335	340	
88	gcg gaa tgc ctc agt	gac agc agc ata ttt	gta cag agt agg aac	tgc	1229
89	Ala Glu Cys Leu Ser	Asp Ser Ser Ile Phe	Val Gln Ser Arg Asn	Cys	
90		345	350	355	360
91	aac ttt cat cat ggc	ttt cat ccc acc act	gtc tgt aag att ccc	agc	1277
92	Asn Phe His His Gly	Phe His Pro Thr Thr	Val Cys Lys Ile Pro	Ser	
93		365	370	375	

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94      agc tgc agc ctc aaa att ttt aac aat cag gag ttt gct cag ctt ctg      1325
95      Ser Cys Ser Leu Lys Ile Phe Asn Asn Gln Glu Phe Ala Gln Leu Leu
96              380              385              390
97      gct caa tct gtc aac cat ggg ttt gag gca gta tat gag ctc acc aaa      1373
98      Ala Gln Ser Val Asn His Gly Phe Glu Ala Val Tyr Glu Leu Thr Lys
99              395              400              405
100     atg tgt acc att cgg atg agt ttt gtc aag ggt tgg gga gca gaa tat      1421
101     Met Cys Thr Ile Arg Met Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr
102             410             415             420
103     cac cgg cag gat gta acc agc acc cca tgt tgg att gag att cat ctt      1469
104     His Arg Gln Asp Val Thr Ser Thr Pro Cys Trp Ile Glu Ile His Leu
105             425             430             435             440
106     cat ggg cct ctt cag tgg ctg gat aaa gtc ctt act cag atg ggc tcc      1517
107     His Gly Pro Leu Gln Trp Leu Asp Lys Val Leu Thr Gln Met Gly Ser
108             445             450             455
109     cct ctg aac ccc ata tct tct gtt tca taa tgcagaagta ttcttttcaa      1567
110     Pro Leu Asn Pro Ile Ser Ser Val Ser
111             460             465
112     ttatatattggt agtggacttg ttttaatttt      1597
114 <210> SEQ ID NO: 2
115 <211> LENGTH: 21
116 <212> TYPE: DNA
117 <213> ORGANISM: Artificial Sequence
118 <220> FEATURE:
119 <223> OTHER INFORMATION: PCR Primer
120 <400> SEQUENCE: 2
121     cagcaagttc tggaccagga a      21
123 <210> SEQ ID NO: 3
124 <211> LENGTH: 23
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: PCR Primer
129 <400> SEQUENCE: 3
130     ccatctgatc atcaggtggc ata      23
132 <210> SEQ ID NO: 4
133 <211> LENGTH: 26
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
137 <223> OTHER INFORMATION: PCR Probe
138 <400> SEQUENCE: 4
139     tccatttcag ctcccagctg atacgc      26
141 <210> SEQ ID NO: 5
142 <211> LENGTH: 19
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: PCR Primer

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147 <400> SEQUENCE: 5
148     gaaggtgaag gtcggagtc                               19
150 <210> SEQ ID NO: 6
151 <211> LENGTH: 20
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: PCR Primer
156 <400> SEQUENCE: 6
157     gaagatggtg atgggatttc                               20
159 <210> SEQ ID NO: 7
160 <211> LENGTH: 20
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <223> OTHER INFORMATION: PCR Probe
165 <400> SEQUENCE: 7
166     caagcttccc gttctcagcc                               20
168 <210> SEQ ID NO: 8
169 <211> LENGTH: 18
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: Antisense Oligonucleotide
174 <400> SEQUENCE: 8
175     ttatcttcac aagtgccca                               18
177 <210> SEQ ID NO: 9
178 <211> LENGTH: 18
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
181 <220> FEATURE:
182 <223> OTHER INFORMATION: Antisense Oligonucleotide
183 <400> SEQUENCE: 9
184     ctaagcagaa gttccaat                               18
186 <210> SEQ ID NO: 10
187 <211> LENGTH: 18
188 <212> TYPE: DNA
189 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
191 <223> OTHER INFORMATION: Antisense Oligonucleotide
192 <400> SEQUENCE: 10
193     tcatacacag gtcctaag                               18
195 <210> SEQ ID NO: 11
196 <211> LENGTH: 18
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Antisense Oligonucleotide
201 <400> SEQUENCE: 11

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Input Set : N:\paola\US09913558.raw

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202	aagaacagat cacaggtg	18
204	<210> SEQ ID NO: 12	
205	<211> LENGTH: 18	
206	<212> TYPE: DNA	
207	<213> ORGANISM: Artificial Sequence	
208	<220> FEATURE:	
209	<223> OTHER INFORMATION: Antisense Oligonucleotide	
210	<400> SEQUENCE: 12	
211	aactcaaagt cagtggct	18
213	<210> SEQ ID NO: 13	
214	<211> LENGTH: 18	
215	<212> TYPE: DNA	
216	<213> ORGANISM: Artificial Sequence	
217	<220> FEATURE:	
218	<223> OTHER INFORMATION: Antisense Oligonucleotide	
219	<400> SEQUENCE: 13	
220	ttcggagacc ttcctgta	18
222	<210> SEQ ID NO: 14	
223	<211> LENGTH: 18	
224	<212> TYPE: DNA	
225	<213> ORGANISM: Artificial Sequence	
226	<220> FEATURE:	
227	<223> OTHER INFORMATION: Antisense Oligonucleotide	
228	<400> SEQUENCE: 14	
229	tttgacacaa atcttcgg	18
231	<210> SEQ ID NO: 15	
232	<211> LENGTH: 18	
233	<212> TYPE: DNA	
234	<213> ORGANISM: Artificial Sequence	
235	<220> FEATURE:	
236	<223> OTHER INFORMATION: Antisense Oligonucleotide	
237	<400> SEQUENCE: 15	
238	acaatcgctt tactgctg	18
240	<210> SEQ ID NO: 16	
241	<211> LENGTH: 18	
242	<212> TYPE: DNA	
243	<213> ORGANISM: Artificial Sequence	
244	<220> FEATURE:	
245	<223> OTHER INFORMATION: Antisense Oligonucleotide	
246	<400> SEQUENCE: 16	
247	atcaccttgt ttccagcc	18
249	<210> SEQ ID NO: 17	
250	<211> LENGTH: 18	
251	<212> TYPE: DNA	
252	<213> ORGANISM: Artificial Sequence	
253	<220> FEATURE:	
254	<223> OTHER INFORMATION: Antisense Oligonucleotide	
255	<400> SEQUENCE: 17	
256	catttctcct cctcatca	18

VERIFICATION SUMMARY

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Input Set : N:\paola\US09913558.raw

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